Numerical Clamping of the Concentrations of Species Using Response Data from Impulse Perturbations: A New Method to Probe Reaction Networks

We are interested in obtaining information about a system by clamping (holding constant) the concentrations of selected species. The method outlined below accomplishes this by utilizing the responses of a system to external (delta function) perturbations of the concentrations in time Using this method we can isolate a segment of a reaction network and study the interactions between its species or clamp a (or several) species and observe its influence on a reactions.. We can isolate a few, two or even one species (and observe its exponential decay).

The idea, which may be patentable, is based on time-dependent responses of a system and uses linearization of the kinetics.Consider a species X_p that we want to investigate. We perturb it (e.g. using a jump in conentration) and observe the time-dependent responses in all species that we can measure. (In all that follows, we restrict attention to deviations from stationary state, denoted δX, and assume the linearized kinetic equations hold.). Assume that the perturbation causes responses in many species and that we believe the responses of some of these species originate from a single species X_q (i.e.X_q may be a branch point in a chain of reactions). We would like to test this hypothesis by eliminating the response from X_q and the responses in all species that are caused by X_q from the original time series in which X_p is perturbed. For this purpose, we perturb X_q with a delta function (i.e. concetration jump) and monitor the responses in all species. These responses will be used to reconstruct (numerically) the waveform of δX_q in the original experiment and the responses due to its waveform in other species. These reconstructed waveforms are then subtracted from the original time series, thereby eliminating δX_q (i.e. clamping the concentration of X_q) and its influence on other species.

We perturb the concentration of X_p with a pulse (which steps or jumps the concentration). This perturbation induces responses in other species, not necessarily pulses; we denote the deviations of the concentrations of species from the stationary state as $g_i\left(k\right)$. We want to hold concentration X_q constant, i.e. δX_q=0, and observe its effect on the original time series. For this purpose we perturb X_q also with a step change in concentration. This causes other nearby species to vary; we record the responses. Using this step perturbation of X_q we reconstruct the time series of X_q when X_p was perturbed. First we normalize the perturbed time series for the perturbation of X_q,which we denote $x^{(q)}$ ($x^{(q)}$ is a vector and $x_i^{(q)}$ denotes the i^{th} species).

$$y^{(q)}\left(k\right) = \frac{1}{x_q^{(q)}\left(1\right)} x^{(q)}\left(k\right),$$

i.e.$y_q^{(q)}\left(1\right) = 1$. Here and in the following we consider time series that are sampled at times $k\Delta t$, $k = 1, 2, ..., N$. Then we construct the waveform $g_q\left(k\right)$

and the responses due to it. The construction is recursive. First, we scale the solution $y^{(q)}(k)$ so that its initial point lies on the curve g_q

$$\overline{y}(k) = g_q(1)\, y^{(q)}(k)$$

Then at each time step we consider a small delta function perturbation of X_q that pushes the solution onto the required waveform $g_q(k)$. The solution is the sum of these scaled, translated solutions (since the system is assumed to be linear):

$$\begin{aligned}
FOR\ k &= 2:N \\
\alpha_q &= g_q(k) - \overline{y}_q(k) \\
FOR\ j &= k:N \\
\overline{y}(j) &= \overline{y}(j) + \alpha_q y^{(q)}(j-k+1) \\
& END\ j \\
& END\ k
\end{aligned}$$

This solution is subtracted from the original time series (in which X_p was perturbed). The result is the original time series with held constant.

For the general case in which a few species q are to be held constant, we sum over these species (q in the above expressions).